

## SEQUENCE LISTING

<110> Rhône-Poulenc Rorer

<120> MEKK1-interacting FHA protein 1 (MIF1)

<130> sequences

<140>

<141>

<150> 93590

<151> 1998-07-21

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 1553

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (2)..(1174)

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ccc tcc tcc agt gag aaa aag aag gta tcc aaa gcc ccc agc act cct 97  
Pro Ser Ser Ser Glu Lys Lys Lys Val Ser Lys Ala Pro Ser Thr Pro  
20 25 30

gtg cca ccc agc cca gcc cca gcc cct gga ctc acc aag cgt gtg aag 145  
Val Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys  
35 40 45

aag agt aaa cag cca ctt cag gtg acc aag gat ctg ggc cgc tgg aag 193  
Lys Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys  
50 55 60

cct gca aat gac ctc ctg ctc ata aat gct gtg ttg cag acc aac gac 241  
Pro Ala Asn Asp Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp

65

70

75

80

ctg acc tcc gtc cac ctg ggc gtg aaa ttc agc tgc cgc ttc acc ctt 289  
 Leu Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu  
 85 90 95

cgg gag gtc cag gag cgt tgg tac gcc ctg ctc tac gat cct gtc atc 337  
 Arg Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile  
 100 105 110

tcc aag ttg gcc tgt cag gcc atg agg cag ctg cac cca gag gct att 385  
 Ser Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile  
 115 120 125

gca gcc atc cag agc aag gcc ctg ttt agc aag gct gag gag cag ctg 433  
 Ala Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu  
 130 135 140

ctg agc aaa gtg gga tcg acc agc cag ccc acc ttg gag acc ttc cag 481  
 Leu Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln  
 145 150 155 160

gac ctg ctg cac aga cac cct gat gcc ttc tac ctg gcc cgt acc gcg 529  
 Asp Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala  
 165 170 175

aag gcc ctg cag gcc cac tgg cag ctc atg aag cag tat tac ctg ctg 577  
 Lys Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu  
 180 185 190

gag gac cag aca gtg cag ccg ctg ccc aaa ggg gac caa gtg ctg aac 625  
 Glu Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn  
 195 200 205

ttc tct gat gca gag gac ctg att gat gac agt aag ctc aag gac atg 673  
 Phe Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met  
 210 215 220

cga gat gag gtc ctg gaa cat gag ctg atg gtg gct gac cgg cgc cag 721  
 Arg Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln  
 225 230 235 240

aag cga gag att cgg cag ctg gaa cag gaa ctg cat aag tgg cag gtg 769  
 Lys Arg Glu Ile Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val  
 245 250 255

ct a gt gac agc atc aca ggc atg agc tct ccg gac ttc gac aac cag	817		
Leu Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln			
260	265	270	
aca ct gca gt gctg cgg ggc cgc atg gt gctg tac ctg atg cgc tcg	865		
Thr Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser			
275	280	285	
cgt gag atc acc ctg ggc aga gca acc aag gat aac cag att gat gt g	913		
Arg Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val			
290	295	300	
gac ct g tct ctg gag ggt ccg gcc tgg aag ata tcc ccg aaa caa gg t	961		
Asp Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly			
305	310	315	320
gtc atc aag ctg aag aac aac ggt gat ttc ttc att gcc aat gag gg t	1009		
Val Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly			
325	330	335	
cga cgg ccc atc tac atc gat gga cgg ccg gt gctc tgt ggc tcc aaa	1057		
Arg Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys			
340	345	350	
tgg cgc ctc agc aac aac tct gt gtc gag atc gcc agc ctg cga tt c	1105		
Trp Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe			
355	360	365	
gtc ttc ctt atc aac cag gac ctc att gcc ctc atc agg gct gag gct	1153		
Val Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala			
370	375	380	
gcc aag atc aca cca cag tga ggaatggtgg caggactcgt gggccctctc	1204		
Ala Lys Ile Thr Pro Gln			
385	390		
cggcctgttt cccctgccac tccagccccc ttgagctggg aactcaggct cctggaaaaa 1264			
cctgggcagt gggaggctca gctgcgggccc attgatttga gccttgagg gaggataggg 1324			
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1553

&lt;210&gt; 2

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 2

Asn Ser Ala Arg Gly Gly Val Glu Pro Gly Arg Cys Ser Gly Ser Glu

1

5

10

15

Pro Ser Ser Ser Glu Lys Lys Val Ser Lys Ala Pro Ser Thr Pro

20

25

30

Val Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys

35

40

45

Lys Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys

50

55

60

Pro Ala Asn Asp Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp

65

70

75

80

Leu Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu

85

90

95

Arg Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile

100

105

110

Ser Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile

115

120

125

Ala Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu

130

135

140

Leu Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln

145

150

155

160

Asp Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala

165

170

175

Lys Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu

180

185

190

Glu Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn

195

200

205

Phe Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met  
 210 215 220

Arg Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln  
 225 230 235 240

Lys Arg Glu Ile Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val  
 245 250 255

Leu Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln  
 260 265 270

Thr Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser  
 275 280 285

Arg Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val  
 290 295 300

Asp Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly  
 305 310 315 320

Val Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly  
 325 330 335

Arg Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys  
 340 345 350

Trp Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe  
 355 360 365

Val Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala  
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Ala Lys Ile Thr Pro Gln  
 385 390

<210> 3  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

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<223> Description of Artificial Sequence:  
oligonucleotide

<400> 3

gatcctcgag agaattccag gtcctcccg gagatcagct tctgctccat ggtgga

56

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
oligonucleotide

<400> 4

cgggatccat ggacaaagat tctcag

26

<210> 5

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 5

agcttccacc atgtatccgt atgatgtgcc tgactacgca gaattctctc gag

53

<210> 6

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 6

gatcctcgag agaattctgc gtatcaggc acatcatacg gatacagggt gga

53

&lt;210&gt; 7

&lt;211&gt; 1914

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (147)..(1535)

&lt;400&gt; 7

cgcgagaaaa ttgttggatc tggcagtcta ggaatgaatc tcctctcagc ctttaagctc 60

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accagtggtt ttgggactgt aagagg atg gac aaa gat tct cag ggg ctg cta 173  
Met Asp Lys Asp Ser Gln Gly Leu Leu

1 5

gat tca tcc ctg atg gca tca ggc act gcc agc cgc tca gag gat gag 221  
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu

10 15 20 25

gag tca ctg gca ggg cag aag cga gcc tcc tcc cag gcc ttg ggc acc 269  
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr

30 35 40

atc cct aaa cgg aga agc tcc tcc agg ttc atc aag agg aag aag ttc 317  
Ile Pro Lys Arg Arg Ser Ser Arg Phe Ile Lys Arg Lys Lys Phe

45 50 55

gat gat gag ctg gtg gag agc agc ctg gca aaa tct tct acc cgg gca 365  
Asp Asp Glu Leu Val Glu Ser Ser Leu Ala Lys Ser Ser Thr Arg Ala

60 65 70

aag ggg gcc agt ggg gtg gaa cca ggg cgc tgt tcg ggg agt gaa ccc 413  
Lys Gly Ala Ser Gly Val Glu Pro Gly Arg Cys Ser Gly Ser Glu Pro

75 80 85

tcc tcc agt gag aag aag gta tcc aaa gcc ccc agc act cct gtg 461  
Ser Ser Ser Glu Lys Lys Val Ser Lys Ala Pro Ser Thr Pro Val

90 95 100 105

cca ccc agc cca gcc cca gcc cct gga ctc acc aag cgt gtg aag aag 509  
Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys Lys

110 115 120

agt aaa cag cca ctt cag gtg acc aag gat ctg ggc cgc tgg aag cct	557		
Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys Pro			
125	130	135	
gca gat gac ctc ctg ctc ata aat gct gtg ttg cag acc aac gac ctg	605		
Ala Asp Asp Leu Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp Leu			
140	145	150	
acc tcc gtc cac ctg ggc gtg aaa ttc agc tgc cgc ttc acc ctt cgg	653		
Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu Arg			
155	160	165	
gag gtc cag gag cgt tgg tac gcc ctg ctc tac gat cct gtc atc tcc	701		
Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile Ser			
170	175	180	185
aag ttg gcc tgt cag gcc atg agg cag ctg cac cca gag gct att gca	749		
Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile Ala			
190	195	200	
gcc atc cag agc aag gcc ctg ttt agc aag gct gag gag cag ctg ctg	797		
Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu Leu			
205	210	215	
agc aaa gtg gga tcg acc agc cag ccc acc ttg gag acc ttc cag gac	845		
Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln Asp			
220	225	230	
ctg ctg cac aga cac cct gat gcc ttc tac ctg gcc cgt acc gcg aag	893		
Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala Lys			
235	240	245	
gcc ctg cag gcc cac tgg cag ctc atg aag cag tat tac ctg ctg gag	941		
Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu Glu			
250	255	260	265
gac cag aca gtg cag ccg ctg ccc aaa ggg gac caa gtg ctg aac ttc	989		
Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn Phe			
270	275	280	
tct gat gca gag gac ctg att gat gac agt aag ctc aag gac atg cga	1037		
Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met Arg			
285	290	295	
gat gag gtc ctg gaa cat gag ctg atg gtg gct gac cgg cgc cag aag	1085		
Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln Lys			

300	305	310	
cga gag att cgg cag ctg gaa cag gaa ctg cat aag tgg cag gtg cta			1133
Arg	Glu	Ile	Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val Leu
315	320	325	
gtg gac agc atc aca ggc atg agc tct ccg gac ttc gac aac cag aca			1181
Val	Asp	Ser	Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln Thr
330	335	340	345
ctg gca gtg ctg cgg ggc cgc atg gtg cgg tac ctg atg cgc tcg cgt			1229
Leu	Ala	Val	Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser Arg
350	355	360	
gag atc acc ctg ggc aga gca acc aag gat aac cag att gat gtg gac			1277
Glu	Ile	Thr	Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val Asp
365	370	375	
ctg tct ctg gag ggt ccg gcc tgg aag ata tcc ccg aaa caa ggt gtc			1325
Leu	Ser	Leu	Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly Val
380	385	390	
atc aag ctg aag aac aac ggt gat ttc ttc att gcc aat gag ggt cga			1373
Ile	Lys	Leu	Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly Arg
395	400	405	
cg <sup>g</sup> ccc atc tac atc gat gga cg <sup>g</sup> ccg gtg ctc tgt ggc tcc aaa tgg			1421
Arg	Pro	Ile	Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys Trp
410	415	420	425
cg <sup>c</sup> ctc agc aac aac tct gtg gtg gag atc gcc agc ctg cga ttc gtc			1469
Arg	Leu	Ser	Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe Val
430	435	440	
ttc ctt atc aac cag gac ctc att gcc ctc atc agg gct gag gct gcc			1517
Phe	Leu	Ile	Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala Ala
445	450	455	
aag atc aca cca cag tga ggaatggtgg caggactcgt gggccctctc			1565
Lys	Ile	Thr	Pro Gln
460			
cggcctgttt cccctgccac tccagcccc ttgagctggg aactcaggct cctggaaaaa			1625
cctggggcagt gggaggctca gctgcgggcc attgattga gccttgagg gaggataggg			1685

ctggccttg tgaagccagc agaggctgag aacctcaggc ttccctagat ccagagcccc 1745  
 tccccatctt cctctctcta aaaacaaccc taccggccat tctacccccc attgccacct 1805  
 tcactcctgt gtctccagct gattgcctc agactcttct tttattgtt ttctttgtt 1865  
 aataaaaagc accaggttcc aaagtaaaaa aaaaaaaaaa aaactcgag 1914

<210> 8  
 <211> 462  
 <212> PRT  
 <213> homo sapiens

<400> 8  
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 Arg Ala Ser Ser Gln Ala Leu Gly Thr Ile Pro Lys Arg Arg Ser Ser  
 35 40 45  
 Ser Arg Phe Ile Lys Arg Lys Lys Phe Asp Asp Glu Leu Val Glu Ser  
 50 55 60  
 Ser Leu Ala Lys Ser Ser Thr Arg Ala Lys Gly Ala Ser Gly Val Glu  
 65 70 75 80  
 Pro Gly Arg Cys Ser Gly Ser Glu Pro Ser Ser Ser Glu Lys Lys Lys  
 85 90 95  
 Val Ser Lys Ala Pro Ser Thr Pro Val Pro Pro Ser Pro Ala Pro Ala  
 100 105 110  
 Pro Gly Leu Thr Lys Arg Val Lys Lys Ser Lys Gln Pro Leu Gln Val  
 115 120 125  
 Thr Lys Asp Leu Gly Arg Trp Lys Pro Ala Asp Asp Leu Leu Leu Ile  
 130 135 140  
 Asn Ala Val Leu Gln Thr Asn Asp Leu Thr Ser Val His Leu Gly Val  
 145 150 155 160  
 Lys Phe Ser Cys Arg Phe Thr Leu Arg Glu Val Gln Glu Arg Trp Tyr

165

170

175

Ala Leu Leu Tyr Asp Pro Val Ile Ser Lys Leu Ala Cys Gln Ala Met  
 180 185 190

Arg Gln Leu His Pro Glu Ala Ile Ala Ala Ile Gln Ser Lys Ala Leu  
 195 200 205

Phe Ser Lys Ala Glu Glu Gln Leu Leu Ser Lys Val Gly Ser Thr Ser  
 210 215 220

Gln Pro Thr Leu Glu Thr Phe Gln Asp Leu Leu His Arg His Pro Asp  
 225 230 235 240

Ala Phe Tyr Leu Ala Arg Thr Ala Lys Ala Leu Gln Ala His Trp Gln  
 245 250 255

Leu Met Lys Gln Tyr Tyr Leu Leu Glu Asp Gln Thr Val Gln Pro Leu  
 260 265 270

Pro Lys Gly Asp Gln Val Leu Asn Phe Ser Asp Ala Glu Asp Leu Ile  
 275 280 285

Asp Asp Ser Lys Leu Lys Asp Met Arg Asp Glu Val Leu Glu His Glu  
 290 295 300

Leu Met Val Ala Asp Arg Arg Gln Lys Arg Glu Ile Arg Gln Leu Glu  
 305 310 315 320

Gln Glu Leu His Lys Trp Gln Val Leu Val Asp Ser Ile Thr Gly Met  
 325 330 335

Ser Ser Pro Asp Phe Asp Asn Gln Thr Leu Ala Val Leu Arg Gly Arg  
 340 345 350

Met Val Arg Tyr Leu Met Arg Ser Arg Glu Ile Thr Leu Gly Arg Ala  
 355 360 365

Thr Lys Asp Asn Gln Ile Asp Val Asp Leu Ser Leu Glu Gly Pro Ala  
 370 375 380

Trp Lys Ile Ser Arg Lys Gln Gly Val Ile Lys Leu Lys Asn Asn Gly  
 385 390 395 400

Asp Phe Phe Ile Ala Asn Glu Gly Arg Arg Pro Ile Tyr Ile Asp Gly  
 405 410 415

Arg Pro Val Leu Cys Gly Ser Lys Trp Arg Leu Ser Asn Asn Ser Val  
420 425 430

Val Glu Ile Ala Ser Leu Arg Phe Val Phe Leu Ile Asn Gln Asp Leu  
435 440 445

Ile Ala Leu Ile Arg Ala Glu Ala Ala Lys Ile Thr Pro Gln  
450 455 460

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 9

ctattcgatg atgaagatac ccc

23

<210> 10

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 10

cgcggagaaa ttgttggaa

18

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 11

ccgatatcgc acttggtccc ctttgg

26

<210> 12

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 12

agcttccacc atggagcaga agctgatctc cgaggaggac ctggaattct ctcgag

56